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RAW SEQUENCE LISTING

DATE: 06/26/2001

PATENT APPLICATION: US/09/766,396

TIME: 15:11:59

Input Set : N:\Crf3\RULE60\09766396.txt

Output Set: N:\CRF3\06262001\I766396.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Sutcliffe, Gregor J.

7 de Lecea, Luis

8 Siggins, George R.

9 Henriksen, Steven J.

11 (ii) TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,

12 COMPOSITIONS AND METHODS

14 (iii) NUMBER OF SEQUENCES: 26

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE

18 (B) STREET: 10666 North Torrey Pines Road, TPC-8

19 (C) CITY: La Jolla

20 (D) STATE: California

21 (E) COUNTRY: US

22 (F) ZIP: 92037

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/766,396

C--> 32 (B) FILING DATE: 18-Jan-2001

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 08/857,389

37 (B) FILING DATE:

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Schmonsees, William

43 (B) REGISTRATION NUMBER: 31,796

44 (C) REFERENCE/DOCKET NUMBER: 22908-0002

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: (415) 324-7041

48 (B) TELEFAX: (415) 324-0638

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 438 base pairs

55 (B) TYPE: nucleic acid

56 (C) STRANDEDNESS: single

57 (D) TOPOLOGY: linear

59 (ii) MOLECULE TYPE: cDNA

61 (iii) HYPOTHETICAL: NO

63 (iv) ANTI-SENSE: NO

65 (ix) FEATURE:

66 (A) NAME/KEY: CDS

67 (B) LOCATION: 30..368

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70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71      AAAGCACAGA CTTCAAGTTT CCAAGGAGG ATG GGT GGC TGC AGC ACA AGA GGC      53
72                                     Met Gly Gly Cys Ser Thr Arg Gly
73                                     1           5
74      AAG CGG CCG TCA GCC CTC AGT CTG CTG CTG CTG CTG CTC TCG GGC      101
75      Lys Arg Pro Ser Ala Leu Ser Leu Leu Leu Leu Leu Leu Ser Gly
76      10           15           20
77      ATC GCA GCC TCT GCC CTC CCC CTG GAG AGC GGT CCC ACC GGC CAG GAC      149
78      Ile Ala Ala Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp
79      25           30           35           40
80      AGT GTG CAG GAT GCC ACA GGC GGG AGG AGG ACC GGC CTT CTG ACT TTC      197
81      Ser Val Gln Asp Ala Thr Gly Gly Arg Arg Thr Gly Leu Leu Thr Phe
82      45           50           55
83      CTT GCC TGG TGG CAT GAG TGG GCT TCC CAA GAC AGC TCC AGC ACC GCT      245
84      Leu Ala Trp Trp His Glu Trp Ala Ser Gln Asp Ser Ser Ser Thr Ala
85      60           65           70
86      TTC GAA GGG GGT ACC CCG GAG CTG TCT AAG CGG CAG GAA AGA CCA CCC      293
87      Phe Glu Gly Gly Thr Pro Glu Leu Ser Lys Arg Gln Glu Arg Pro Pro
88      75           80           85
89      CTC CAG CAG CCC CCA CAC CGG GAT AAA AAG CCC TGC AAG AAC TTC TTC      341
90      Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro Cys Lys Asn Phe Phe
91      90           95           100
92      TGG AAA ACC TTC TCC TCG TGC AAG TAGCCCGAGC CTGACCGGAG CCTGACCGGC      395
93      Trp Lys Thr Phe Ser Ser Cys Lys
94      105           110
95      CACCCTGTGA ATGCAGCCGT GGCCTGAATA AAGAGTGTCA AGT      438
96      (2) INFORMATION FOR SEQ ID NO: 2:
97      (i) SEQUENCE CHARACTERISTICS:
98      (A) LENGTH: 112 amino acids
99      (B) TYPE: amino acid
100     (D) TOPOLOGY: linear
101     (ii) MOLECULE TYPE: protein
102     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
103     Met Gly Gly Cys Ser Thr Arg Gly Lys Arg Pro Ser Ala Leu Ser Leu
104     1           5           10           15
105     Leu Leu Leu Leu Leu Leu Ser Gly Ile Ala Ala Ser Ala Leu Pro Leu
106     20           25           30
107     Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln Asp Ala Thr Gly Gly
108     35           40           45
109     Arg Arg Thr Gly Leu Leu Thr Phe Leu Ala Trp Trp His Glu Trp Ala
110     50           55           60
111     Ser Gln Asp Ser Ser Ser Thr Ala Phe Glu Gly Gly Thr Pro Glu Leu
112     65           70           75           80
113     Ser Lys Arg Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp
114     85           90           95
115     Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
116     100          105          110
117     (2) INFORMATION FOR SEQ ID NO: 3:
118     (i) SEQUENCE CHARACTERISTICS:

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145      (A) LENGTH: 110 amino acids
146      (B) TYPE: amino acid
147      (D) TOPOLOGY: linear
149      (ii) MOLECULE TYPE: protein
151      (v) FRAGMENT TYPE: C-terminal
155      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
157      Gln Cys Ala Leu Ala Ala Leu Cys Ile Val Leu Ala Leu Gly Gly Val
158      1          5          10          15
160      Thr Gly Ala Pro Ser Asp Pro Arg Leu Arg Gln Phe Leu Gln Lys Ser
161      20          25          30
163      Leu Ala Ala Ala Thr Gly Lys Gln Glu Leu Ala Lys Tyr Phe Leu Ala
164      35          40          45
166      Glu Leu Leu Ser Glu Pro Asn Gln Thr Glu Asn Asp Ala Leu Glu Pro
167      50          55          60
169      Glu Asp Leu Pro Gln Ala Ala Glu Gln Asp Glu Met Arg Leu Glu Leu
170      65          70          75          80
172      Gln Arg Ser Ala Asn Ser Asn Pro Ala Met Ala Pro Arg Glu Arg Lys
173      85          90          95
174      Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
175      100         105         110
177 (2) INFORMATION FOR SEQ ID NO: 4:
179      (i) SEQUENCE CHARACTERISTICS:
180          (A) LENGTH: 427 base pairs
181          (B) TYPE: nucleic acid
182          (C) STRANDEDNESS: single
183          (D) TOPOLOGY: linear
185      (ii) MOLECULE TYPE: cDNA
187      (iii) HYPOTHETICAL: NO
189      (iv) ANTI-SENSE: NO
192      (ix) FEATURE:
193          (A) NAME/KEY: CDS
194          (B) LOCATION: 25..354
197      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
199      GCACGAGGCT CAGCACGTCC GAGG ATG ATG GGT GGC CGA GGC ACA GGA GGC      51
200          Met Met Gly Gly Arg Gly Thr Gly Gly
201          1          5
203      AAG TGG CCC TCA GCC TTC GGG CTG CTG CTG CTC TGG GGG GTC GCA GCC      99
204      Lys Trp Pro Ser Ala Phe Gly Leu Leu Leu Leu Trp Gly Val Ala Ala
205      10          15          20          25
207      TCC GCC CTT CCC CTG GAG AGT GGC CCT ACT GGC CAG GAC AGT GTG CAG      147
208      Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
209      30          35          40
211      GAA GCC ACC GAG GGG AGG AGC GGC CTT CTG ACT TTC CTT GCC TGG TGG      195
212      Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp
213      45          50          55
215      CAC GAG TGG GCT TCC CAA GCC AGC TCC AGC ACC CCC GTC GGA GGG GGT      243
216      His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly
217      60          65          70
219      ACC CCC GGG CTG TCC AAG AGC CAG GAA AGG CCA CCC CCC CAA CAG CCC      291

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220 Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro
221      75      80      85
223 CCA CAC CTG GAT AAA AAG CCC TGC AAG AAC TTC TTC TGG AAA ACC TTC      339
224 Pro His Leu Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe
225  90      95      100      105
226 TCC TCG TGC AAG TAACCCACC CTGGGCATAG CACCCTGGCC ACCCTGTGAG      391
227 Ser Ser Cys Lys
W--> 228      110
230 ATGCCAACGA GACCTGAATA AAGACTGTCA ATCAAC      427
233 (2) INFORMATION FOR SEQ ID NO: 5:
235      (i) SEQUENCE CHARACTERISTICS:
236          (A) LENGTH: 109 amino acids
237          (B) TYPE: amino acid
238          (D) TOPOLOGY: linear
240      (ii) MOLECULE TYPE: protein
242      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
244 Met Met Gly Gly Arg Gly Thr Gly Gly Lys Trp Pro Ser Ala Phe Gly
245  1      5      10      15
247 Leu Leu Leu Leu Trp Gly Val Ala Ala Ser Ala Leu Pro Leu Glu Ser
248      20      25      30
250 Gly Pro Thr Gly Gln Asp Ser Val Gln Glu Ala Thr Glu Gly Arg Ser
251      35      40      45
253 Gly Leu Leu Thr Phe Leu Ala Trp Trp His Glu Trp Ala Ser Gln Ala
254      50      55      60
256 Ser Ser Ser Thr Pro Val Gly Gly Gly Thr Pro Gly Leu Ser Lys Ser
257  65      70      75      80
259 Gln Glu Arg Pro Pro Pro Gln Gln Pro Pro His Leu Asp Lys Lys Pro
260      85      90      95
262 Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
263      100      105
266 (2) INFORMATION FOR SEQ ID NO: 6:
268      (i) SEQUENCE CHARACTERISTICS:
269          (A) LENGTH: 85 amino acids
270          (B) TYPE: amino acid
271          (D) TOPOLOGY: linear
273      (ii) MOLECULE TYPE: protein
275      (v) FRAGMENT TYPE: C-terminal
279      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
281 Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
282  1      5      10      15
283 Asp Ala Thr Gly Gly Arg Arg Thr Gly Leu Leu Thr Phe Leu Ala Trp
284      20      25      30
286 Trp His Glu Trp Ala Ser Gln Asp Ser Ser Ser Thr Ala Phe Glu Gly
287      35      40      45
289 Gly Thr Pro Glu Leu Ser Lys Arg Gln Glu Arg Pro Pro Leu Gln Gln
290      50      55      60
292 Pro Pro His Arg Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr
293  65      70      75      80
295 Phe Ser Ser Cys Lys

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TIME: 15:11:59

Input Set : N:\Crif3\RULE60\09766396.txt

Output Set: N:\CRF3\06262001\I766396.raw

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296                               85
298 (2) INFORMATION FOR SEQ ID NO: 7:
300   (i) SEQUENCE CHARACTERISTICS:
301       (A) LENGTH: 29 amino acids
302       (B) TYPE: amino acid
303       (D) TOPOLOGY: linear
305   (ii) MOLECULE TYPE: protein
307   (v) FRAGMENT TYPE: C-terminal
311   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
313   Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro
314   1      5      10      15
316   Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
317   20      25
319 (2) INFORMATION FOR SEQ ID NO: 8:
321   (i) SEQUENCE CHARACTERISTICS:
322       (A) LENGTH: 14 amino acids
323       (B) TYPE: amino acid
324       (D) TOPOLOGY: linear
326   (ii) MOLECULE TYPE: protein
328   (v) FRAGMENT TYPE: C-terminal
332   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
334   Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
335   1      5      10
337 (2) INFORMATION FOR SEQ ID NO: 9:
339   (i) SEQUENCE CHARACTERISTICS:
340       (A) LENGTH: 13 amino acids
341       (B) TYPE: amino acid
342       (D) TOPOLOGY: linear
344   (ii) MOLECULE TYPE: protein
346   (v) FRAGMENT TYPE: internal
350   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
352   Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp
353   1      5      10
355 (2) INFORMATION FOR SEQ ID NO: 10:
357   (i) SEQUENCE CHARACTERISTICS:
358       (A) LENGTH: 84 amino acids
359       (B) TYPE: amino acid
360       (D) TOPOLOGY: linear
362   (ii) MOLECULE TYPE: protein
364   (v) FRAGMENT TYPE: C-terminal
368   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
370   Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
371   1      5      10      15
373   Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp
374   20      25      30
376   His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly
377   35      40      45
379   Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro
380   50      55      60

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/766,396

DATE: 06/26/2001

TIME: 15:12:00

Input Set : N:\Crf3\RULE60\09766396.txt

Output Set: N:\CRF3\06262001\I766396.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4